

SEQUENCE LISTING

<110> Salon et al, John A.

<120> DNA Encoding A Human Melanin Concentrating Hormone Receptor (MCH1) And Uses Thereof

<130> 1795/57453-C/JPW

<140> NotYetKnown

<141> 2001-07-05

<150> 09/610,635

<151> 2000-07-05

<160> 28

<170> PatentIn Ver. 2.1

<210> 1

<211> 1269

<212> DNA

<213> Homo sapiens

<400> 1

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cgcacgggga gcatctccta catcaacatc atcatgcctt cggtgttgcg caccatctgc 360
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<210> 2
<211> 422
<212> PRT
<213> Homo sapiens

<400> 2
Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Met Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415

Thr Glu Ser Lys Gly Thr
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<210> 3
<211> 1214
<212> DNA
<213> Rattus norvegicus

<400> 3
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tgagattaaa cccaggcta ccctggaga atgcagaggc tggaggctgg gggctttag 1200
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1214

<210> 4

<211> 353

<212> PRT

<213> Rattus norvegicus

<400> 4

Met Asp Leu Gln Thr Ser Leu Leu Ser Thr Gly Pro Asn Ala Ser Asn
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Ile Ser Asp Gly Gln Asp Asn Leu Thr Leu Pro Gly Ser Pro Pro Arg
20 25 30

Thr Gly Ser Val Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
35 40 45

Thr Ile Cys Leu Leu Gly Ile Val Gly Asn Ser Thr Val Ile Phe Ala
50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Ser Asn Val Pro Asp Ile
65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
100 105 110

10025314-122003

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Thr Ile Asp Arg Tyr Leu Ala
130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Met Ala
145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile
210 215 220

Thr Ala Ala Tyr Val Lys Ile Leu Gln Arg Met Thr Ser Ser Val Ala
225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Thr
325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
340 345 350

Thr

T O O D E P T H

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<210> 5
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 5
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<210> 6
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 6
tagcggtaaa tggccatggc ggtcag 26

<210> 7
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 7
ctcctgggca tgcccttcat gatccaccag ctcatgggca atggg 45

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 8
cttcttaggcc tgtacggaag tgtta 25
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<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 9
gttgggttt gtccaaactc atcaatg 27

<210> 10
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 10
cgcgatcca ttatgtctgc actccgaagg aaatttg 37

<210> 11
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 11
cgcgaattct tatgtgaagc gatcagagtt catttttc 38

<210> 12
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 12
gcgggatccg ctatggctgg tgattctagg aatg 34

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 13
ccggaattcc cctcacacccg agccccctgg 29

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 14
tcagctcggt tgtgggagca 20

<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer/probe

<400> 15
cttggacttc ttcacgac 18

<210> 16
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: mutated human MCH1

<400> 16

Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Thr Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
85 90 95

Gly Ser Pro Pro
100

<210> 17

<211> 100

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human
MCH1

<400> 17

Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Prc
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala

Gly Ser Pro Pro
100

<210> 18

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 18

cggcactggc tgggcggacc tggaagcctc g

31

<210> 19

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 19

cgaggcgttcc aggtccgccc agccagtgcc g

31

<210> 20

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 20

atgtcagtgg gagccgcgaa gaagggagtg gg

32

<210> 21

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 21

cccaactccct tcttcgcggc tccccactgac at

32

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 22

taatgtgtct aggtggcgtc agtgggagcc atg

33

<210> 23

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 23

catggctccc actgacgcca cctagacaca tta

33

<210> 24

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 24

tgcacactaag cttcaactggc tggatggacc tggaagc

37

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 25

gcccgaggaga aagaggagat ctac

24

<210> 26

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human
MCH1

<400> 26

Met Ser Val Gly Ala Met Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415

Thr Glu Ser Lys Gly Thr
420

<210> 27

<211> 422

<212> PRT

<213> Artificial Sequence

<220>

-<223> Description of Artificial Sequence: mutated human
MCH1

<400> 27

Met Ser Val Gly Ala Ala Lys Lys Gly Val Gly Arg Ala Val Gly Leu
1 5 10 15

Gly Gly Gly Ser Gly Cys Gln Ala Thr Glu Glu Asp Pro Leu Pro Asp
20 25 30

Cys Gly Ala Cys Ala Pro Gly Gln Gly Gly Arg Arg Trp Arg Leu Pro
35 40 45

Gln Pro Ala Trp Val Glu Gly Ser Ser Ala Arg Leu Trp Glu Gln Ala
50 55 60

Thr Gly Thr Gly Trp Ala Asp Leu Glu Ala Ser Leu Leu Pro Thr Gly
65 70 75 80

Pro Asn Ala Ser Asn Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala
85 90 95

Gly Ser Pro Pro Arg Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met
100 105 110

Pro Ser Val Phe Gly Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser
115 120 125

Thr Val Ile Phe Ala Val Val Lys Lys Ser Lys Leu His Trp Cys Asn
130 135 140

Asn Val Pro Asp Ile Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu
145 150 155 160

Phe Leu Leu Gly Met Pro Phe Met Ile His Gln Leu Met Gly Asn Gly
165 170 175

Val Trp His Phe Gly Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp
180 185 190

Ala Asn Ser Gln Phe Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile
195 200 205

Asp Arg Tyr Leu Ala Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg
210 215 220

Lys Pro Ser Val Ala Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser
225 230 235 240

Phe Ile Ser Ile Thr Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe
245 250 255

Pro Gly Gly Ala Val Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr
260 265 270

Asp Leu Tyr Trp Phe Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu
275 280 285

Pro Phe Val Val Ile Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met
290 295 300

Thr Ser Ser Val Ala Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr
305 310 315 320

Lys Arg Val Thr Arg Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val
325 330 335

Cys Trp Ala Pro Tyr Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser
340 345 350

Arg Pro Thr Leu Thr Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu
355 360 365

Gly Tyr Ala Asn Ser Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys
370 375 380

Glu Thr Phe Arg Lys Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln
385 390 395 400

Gly Gln Leu Arg Ala Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg
405 410 415

Thr Glu Ser Lys Gly Thr
420

<210> 28
<211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: mutated human
MCH1

<400> 28

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Thr Ser Asp Gly Pro Asp Asn Leu Thr Ser Ala Gly Ser Pro Pro Arg
20 25 30

Thr Gly Ser Ile Ser Tyr Ile Asn Ile Ile Met Pro Ser Val Phe Gly
35 40 45

Thr Ile Cys Leu Leu Gly Ile Ile Gly Asn Ser Thr Val Ile Phe Ala
50 55 60

Val Val Lys Lys Ser Lys Leu His Trp Cys Asn Asn Val Pro Asp Ile
65 70 75 80

Phe Ile Ile Asn Leu Ser Val Val Asp Leu Leu Phe Leu Leu Gly Met
85 90 95

Pro Phe Met Ile His Gln Leu Met Gly Asn Gly Val Trp His Phe Gly
100 105 110

Glu Thr Met Cys Thr Leu Ile Thr Ala Met Asp Ala Asn Ser Gln Phe
115 120 125

Thr Ser Thr Tyr Ile Leu Thr Ala Met Ala Ile Asp Arg Tyr Leu Ala
130 135 140

Thr Val His Pro Ile Ser Ser Thr Lys Phe Arg Lys Pro Ser Val Ala
145 150 155 160

Thr Leu Val Ile Cys Leu Leu Trp Ala Leu Ser Phe Ile Ser Ile Thr
165 170 175

Pro Val Trp Leu Tyr Ala Arg Leu Ile Pro Phe Pro Gly Gly Ala Val
180 185 190

Gly Cys Gly Ile Arg Leu Pro Asn Pro Asp Thr Asp Leu Tyr Trp Phe
195 200 205

Thr Leu Tyr Gln Phe Phe Leu Ala Phe Ala Leu Pro Phe Val Val Ile

210

215

220

Thr Ala Ala Tyr Val Arg Ile Leu Gln Arg Met Thr Ser Ser Val Ala
225 230 235 240

Pro Ala Ser Gln Arg Ser Ile Arg Leu Arg Thr Lys Arg Val Thr Arg
245 250 255

Thr Ala Ile Ala Ile Cys Leu Val Phe Phe Val Cys Trp Ala Pro Tyr
260 265 270

Tyr Val Leu Gln Leu Thr Gln Leu Ser Ile Ser Arg Pro Thr Leu Thr
275 280 285

Phe Val Tyr Leu Tyr Asn Ala Ala Ile Ser Leu Gly Tyr Ala Asn Ser
290 295 300

Cys Leu Asn Pro Phe Val Tyr Ile Val Leu Cys Glu Thr Phe Arg Lys
305 310 315 320

Arg Leu Val Leu Ser Val Lys Pro Ala Ala Gln Gly Gln Leu Arg Ala
325 330 335

Val Ser Asn Ala Gln Thr Ala Asp Glu Glu Arg Thr Glu Ser Lys Gly
340 345 350

Thr